1. (Twice amended) A method for determining the type of target nucleic acids in a sample, wherein the method is capable of differentiating free and encapsulated target nucleic acids in the sample, wherein the method comprises

(a) determining a total target nucleic acid content in the sample;

(b) adding a nuclease to the sample to digest free target nucleic acids in the sample to form a nuclease-treated sample;

(c) determining a total target nucleic acid content remaining in the nuclease-treated sample, thereby quantifying the amount of encapsulated target nucleic acids in the sample; and

(d) quantifying the total amount of free target nucleic acid in the sample by subtracting the determined amount of target nucleic acid content in the nuclease-treated sample from the determined amount of total target nucleic acid content in the sample, wherein steps (c) and (d) determine the types of target nucleic acids in the sample.

3. (Twice amended) The method of claim 1, wherein all determining of the target nucleic acids is performed using a nucleic acid amplification assay selected from the group consisting of a polymerase chain reaction (PCR) assay and a reverse transcriptase (RT) PCR assay.

21. (Amended) A method for determining the proportion of infectious pathogens and inactivated pathogens in a sample, wherein the method is capable of